



SEQUENCE LISTING

<110> VETIGEN
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<120> MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS

<130> 053356-5001-US

<140> US 09/319,724
<141> 1999-09-08

<150> EP 96402719.7
<151> 1996-12-12

<160> 14

<170> PatentIn version 3.1

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<212> PRT
<213> Homo sapiens

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Lys Val Lys Leu Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val
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Lys Trp Lys Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr
65 70 75 80

Leu Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe
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Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile
100 105 110

Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu Glu
115 120 125

Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys
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Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe
145 150 155 160

Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile
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Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser
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Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn
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Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp
210 215 220

Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys
225 230 235 240

Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser
245 250 255

Arg Ala Ile Pro Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe
260 265 270

Phe Val Ile Leu Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn
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Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg
290 295 300

Pro Ile Pro Glu Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys
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Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe
325 330 335

Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe
 340 345 350

Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr
 355 360 365

Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln
 370 375 380

Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met
 385 390 395 400

Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe
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Gly Ile Met Cys Gly Ala Ile
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 gatgttaatc taactagtga aggaaagggtg aaactgggttc caaatactaa aatccagatg 180
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gatgaatatg gatggaaaca ggtgcatgga gatgtattta gaccatcaag tcacccactg	300
atattttcct ctctgattgg ttctggatgt cagatatttg ctgtgtctct catcgttatt	360
attgttgcaa tgatagaaga tttatatact gagaggggat caatgctcag tacagccata	420
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caaggaggaa ggagatggat aaagcagatg tttattgggg cattccttat cccagctatg	540
gtgtgtggca ctgccttctt catcaatttc atagccattt attaccatgc ttcaagagcc	600
attccttttg gaacaatggg ggccggttgt tgcactctgt tttttgttat tcttctctta	660
aatcttggtg gtacaatact tggccgaaat ctgtcaggtc agcccaactt tccttgctcg	720
gtcaatgctg tgcctcgtcc tataccggag aaaaaatggg tcatggagcc tgcggttatt	780

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atcctgtgca ttgtgactgt ctgtgtgact attgtgtgca catattttct actaaatgca 960
gaaga 965

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atcttcttgg tgggcttagt ttcaatgatt ttaatgagaa cattaagaaa agattatgct 180
cggtagagta aagaggaaga aatggatgat atggatagag acctaggaga tgaatatgga 240
tggaaacagg tgcattggaga tgtattttaga ccatcaagtc accca 285

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Ser

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<222> (3)..(3)
<223> Xaa can be any amino acid

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gac gag cac gaa cac acg tat caa gat aaa gag gaa gtt gtc tta tgg 95
Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp
20 25 30

atg aat act gtt ggg ccc tac cat aat cgt caa gaa aca tat aag tac 143
Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr
35 40 45

ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa agt atc agt cat tac 191
Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr
50 55 60

cat gaa act ctg gga gaa gca ctt caa ggg gtt gaa ttg gaa ttt agt 239

His	Glu	Thr	Leu	Gly	Glu	Ala	Leu	Gln	Gly	Val	Glu	Leu	Glu	Phe	Ser	
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ggt	ctg	gat	att	aaa	ttt	aaa	gat	gat	gtg	atg	cca	gcc	act	tac	tgt	287
Gly	Leu	Asp	Ile	Lys	Phe	Lys	Asp	Asp	Val	Met	Pro	Ala	Thr	Tyr	Cys	
80					85				90						95	
gaa	att	gat	tta	gat	aaa	gaa	aag	aga	gat	gca	ttt	gta	tat	gcc	ata	335
Glu	Ile	Asp	Leu	Asp	Lys	Glu	Lys	Arg	Asp	Ala	Phe	Val	Tyr	Ala	Ile	
				100					105					110		
aaa	aat	cat	tac	tgg	tac	cag	atg	tac	ata	gat	gat	tta	cca	ata	tgg	383
Lys	Asn	His	Tyr	Trp	Tyr	Gln	Met	Tyr	Ile	Asp	Asp	Leu	Pro	Ile	Trp	
			115					120					125			
ggt	att	ggt	ggt	gag	gct	gat	gaa	aat	gga	gaa	gat	tac	tat	ctt	tgg	431
Gly	Ile	Val	Gly	Glu	Ala	Asp	Glu	Asn	Gly	Glu	Asp	Tyr	Tyr	Leu	Trp	
	130						135					140				
acc	tat	aaa	aaa	ctt	gaa	ata	ggt	ttt	aat	gga	aat	cga	att	ggt	gat	479
Thr	Tyr	Lys	Lys	Leu	Glu	Ile	Gly	Phe	Asn	Gly	Asn	Arg	Ile	Val	Asp	
	145					150					155					
ggt	aat	cta	act	agt	gaa	gga	aag	gtg	aaa	ctg	ggt	cca	aat	act	aaa	527
Val	Asn	Leu	Thr	Ser	Glu	Gly	Lys	Val	Lys	Leu	Val	Pro	Asn	Thr	Lys	
160					165					170					175	
atc	cag	atg	tca	tat	tca	gta	aaa	tgg	aaa	aag	tca	gat	gtg	aaa	ttt	575
Ile	Gln	Met	Ser	Tyr	Ser	Val	Lys	Trp	Lys	Lys	Ser	Asp	Val	Lys	Phe	
			180						185					190		
gaa	gat	cga	ttt	gac	aaa	tat	ctt	gat	ccg	tcc	ttt	ttt	caa	cat	cgg	623
Glu	Asp	Arg	Phe	Asp	Lys	Tyr	Leu	Asp	Pro	Ser	Phe	Phe	Gln	His	Arg	
			195					200					205			
att	cat	tgg	ttt	tca	att	ttc	aac	tcc	ttc	atg	atg	gtg	atc	ttc	ttg	671
Ile	His	Trp	Phe	Ser	Ile	Phe	Asn	Ser	Phe	Met	Met	Val	Ile	Phe	Leu	
	210						215					220				
gtg	ggc	tta	ggt	tca	atg	att	tta	atg	aga	aca	tta	aga	aaa	gat	tat	719
Val	Gly	Leu	Val	Ser	Met	Ile	Leu	Met	Arg	Thr	Leu	Arg	Lys	Asp	Tyr	
	225					230					235					
gct	cgg	tac	agt	aaa	gag	gaa	gaa	atg	gat	gat	atg	gat	aga	gac	cta	767
Ala	Arg	Tyr	Ser	Lys	Glu	Glu	Glu	Met	Asp	Asp	Met	Asp	Arg	Asp	Leu	
240					245					250				255		
gga	gat	gaa	tat	gga	tgg	aaa	cag	gtg	cat	gga	gat	gta	ttt	aga	cca	815
Gly	Asp	Glu	Tyr	Gly	Trp	Lys	Gln	Val	His	Gly	Asp	Val	Phe	Arg	Pro	
				260					265					270		
tca	agt	cac	cca	ctg	ata	ttt	tcc	tct	ctg	att	ggt	tct	gga	tgt	cag	863
Ser	Ser	His	Pro	Leu	Ile	Phe	Ser	Ser	Leu	Ile	Gly	Ser	Gly	Cys	Gln	
			275					280					285			
ata	ttt	gct	gtg	tct	ctc	atc	ggt	att	att	ggt	gca	atg	ata	gaa	gat	911

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Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr	
305 310 315	
gct gct acg tct cca gtg aat ggt tat ttt gga gga agt ctg tat gct	1007
Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala	
320 325 330 335	
aga caa gga gga agg aga tgg ata aag cag atg ttt att ggg gca ttc	1055
Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe	
340 345 350	
ctt atc cca gct atg gtg tgt ggc act gcc ttc ttc atc aat ttc ata	1103
Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile	
355 360 365	
gcc att tat tac cat gct tca aga gcc att cct ttt gga aca atg gtg	1151
Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val	
370 375 380	
gcc gtt tgt tgc atc tgt ttt ttt gtt att ctt cct cta aat ctt gtt	1199
Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val	
385 390 395	
ggt aca ata ctt ggc cga aat ctg tca ggt cag ccc aac ttt cct tgt	1247
Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys	
400 405 410 415	
cgt gtc aat gct gtg cct cgt cct ata ccg gag aaa aaa tgg ttc atg	1295
Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met	
420 425 430	
gag cct gcg gtt att gtt tgc ctg ggt gga att tta cct ttt ggt tca	1343
Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser	
435 440 445	
atc ttt att gaa atg tat ttc atc ttc acg tct ttc tgg gca tat aag	1391
Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys	
450 455 460	
atc tat tat gtc tat ggc ttc atg atg ctg gtg ctg gtt atc ctg tgc	1439
Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys	
465 470 475	
att gtg act gtc tgt gtg act att gtg tgc aca tat ttt cta cta aat	1487
Ile Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn	
480 485 490 495	
gca gaa gat tac cgg tgg caa tgg aca agt ttt ctc tct gct gca tca	1535
Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser	
500 505 510	
act gca atc tat gtt tac atg tat tcc ttt tac tac tat ttt ttc aaa	1583

Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys
 515 520 525

aca aag atg tat ggc tta ttt caa aca tca ttt tac ttt gga tat atg 1631
 Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met
 530 535 540

gcg gta ttt agc aca gcc ttg ggg ata atg tgt gga gcg att ggt tac 1679
 Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr
 545 550 555

atg gga aca agt gcc ttt gtc cga aaa atc tat act aat gtg aaa att 1727
 Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile
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 Asp

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 35 40 45

Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr His
 50 55 60

Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser Gly
 65 70 75 80

Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys Glu
 85 90 95

Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile Lys
 100 105 110

Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly
115 120 125

Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr
130 135 140

Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp Val
145 150 155 160

Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr Lys Ile
165 170 175

Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe Glu
180 185 190

Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg Ile
195 200 205

His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu Val
210 215 220

Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala
225 230 235 240

Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu Gly
245 250 255

Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro Ser
260 265 270

Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile
275 280 285

Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp Leu
290 295 300

Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr Ala
305 310 315 320

Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg
325 330 335

C1
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Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe Leu
340 345 350

Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala
355 360 365

Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val Ala
370 375 380

Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val Gly
385 390 395 400

Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg
405 410 415

Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met Glu
420 425 430

Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile
435 440 445

Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile
450 455 460

Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile
465 470 475 480

Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala
485 490 495

Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr
500 505 510

Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr
515 520 525

Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala
530 535 540

Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr Met
545 550 555 560

Sw
86
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Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile Asp
565 570 575
